

I hereby state that the amendments included in the substitute Sequence Listing are supported in the application, as filed, at least in the original Sequence Listing, for the amendments to SEQ ID NOs:1, 3, 5, 6, 7, 8, 11, 12, 15, 16, 23, 24, 28, 31, 32, 35, 36, and 39. The amendments to <110> and <140> in the Sequence Listing reflect U.S. filing information. Thus, the substitute Sequence Listing does not include new matter.

A copy of the substitute Sequence Listing in computer readable form, along with the required Statement under 37 C.F.R. 1.821(g) and 1.825(b), are filed simultaneously herewith and serve as the response to the NOTIFICATION OF MISSING REQUIREMENTS UNDER 35 U.S.C. 371 (copy enclosed).

Please charge any necessary fees or credits to Deposit Account 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,



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Enclosures: copy of NOTIFICATION OF MISSING REQUIREMENTS UNDER 35 U.S.C. 371
substitute Sequence Listing

FIGURE 1

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MITALDLYVLTAVVPLYVAMTILAYGVSVRWKIFTPDQCSGINREVALFAVPLLSHFHS
MITLTDFYHVTAMVPLYVAMTILAYGVSVKWKIFSPDQCSGINREVALFAVPLLSHFHS
MITGKDIYDFAAIVPLYVAMTILAYGVSVRWKIFTPDQCSGINREVALFAVPLLSHFHS
MITGKDIYDLAAVPLYVAMTILAYGVSVRWKIFTPDQCSGINREVALFAVPLLSHFHS
MITGKDIYDLAAVPLYVAMTILAYGVSVRWKIFTPDQCSGINREVALFAVPLLSHFHS
MITGKDIYDLAAVPLYVAMTILAYGVSVRWKIFTPDQCSGINREVALFAVPLLSHFHS
MITRADEFYHVTAMVPLYVAMTILAYGVSVKWKIFTPDQCSGINREVALFAVPLLSHFHS
1
60

* * * * * *** * * * * *
TNDPFAMNLRFLAADTLQKVAIVALLALASGLSPRALG-----LDWSITILFSL
SNPYEMNLRFLAADTLQKIIILVLLAVW-----SNITKRG-----CLEWATITLFSLS
SNDRPYAMNHRFLAADCLOKVVILGALFLWNT----FTKHG-----SLDWITITLFSLS
TNDPYANDYRFLAADSLOKVLILAAALAVHNNVLSRYRCRGTEAGEASSLDWITITLFSLS
SNDRPYAMNHRFLAADSLOKVVILAAALFLMOA----FSRRG-----SLEWITITLFSLS
ANNPYAMNLRFLAADSLOKVVILSLLFLW-----CKLSRNG-----SLDWITITLFSLS
61
120

*****
TLPNTLVNGIPLLRGMYGASSAGTLMVQVVVLOCIIWYTLMLFLFEYRAARALVLDQFPD
TLPNTLVNGIPLLRGMYGDFS-GSLMWQIVVVLQCIIWYTLMLFLFEYRGARMLISQFP-
TLPNTLVNGIPLLRAMYGDFS-GSLMWQIVVVLQSVIWWYTLMLFMFEYRGAKLLITISQFP-
TLPNTLVNGIPLLRAMYGDFS-GSLMWQIVVVLQSVIWWYTLMLFLFEYRGAKALISQFP
TLPNTLVNGIPLLRAMYGDFS-GNLMWQIVVVLQSVIWWYTLMLFLFEYRGAKLLISQFP-
TLPNTLVNGIPLLRAMYGDFS-GNLMWQIVVVLQSVIWWYTLMLFLFEYRGAKLLISQFP-
180
121

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FIGURE 1 CONTINUED

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SEQ ID NO:14      GAAASIVSFRVDSVSLARGDVELEAEPDGVAGAVSSRGDAGVRVTVRKSTSSRS
SEQ ID NO:30      DTAASIVSIHVSDVMSLD-GROPLETEAEI-----KEDGKLHVTVRKSNASRS
SEQ ID NO:34      ETAGSITSFRVDSVSLN-GREPLQTD AEI-----GEDGKLHVTVRKSNASRS
SEQ ID NO:38      DVGASIASFRVDSVSLN-GREALHADA EV-----GRDGRVHVTVRRSASGST
SEQ ID NO:43      ETAGSITSFRVDSVSLN-GREPLQTD AEI-----GDDGKLHVTVRRSASRS
SEQ ID NO:44      DTAGSIVSIHVSDVMSLD-GROPLETEAEI-----KEDGKLHVTVRRSASRS
240

181
SEQ ID NO:14      EACSHSHSQ-----TMQPRVSNLSGV E IYSLQSSRNPTPRGSSFNHADFFNIYGA-
SEQ ID NO:30      DI---FRR-----SQGLSSTTPRPSNLTNAE IYSLQSSRNPTPRGSSFNHTDFYMSMAAG-
SEQ ID NO:34      MIS-SFNKSHLTSM-----TPRASNLTVGE IYSLQSSRNPTPRGSSFNQTDYAMF-ASK
SEQ ID NO:38      TGGHAGRSGLYRGASNAMPTRASNLTVGE IYSLQTSREPTPRQSSFNQDSDFYMFNGSK
SEQ ID NO:43      MIS-SFNKSHGGLNSSMITPRASNLTVGE IYSLQSSRNPTPRASSFNQTDYAMFNASK
SEQ ID NO:44      DI---YSRR-----SQGLSAT-PRPSNLTNAE IYSLQSSRNPTPRGSSFNHTDFYMSMAAG-
240

241
SEQ ID NO:14      ---AKG-----GGAAGDE-----
SEQ ID NO:30      ---G-RNSNF-----GASD-YIGLSASRGTPRPSNYDEDGKPK-K-----
SEQ ID NO:34      APSPKHYTNSFQSNNGGIG-DVYSLQSSKGATPRTSNFEELMKVHKK--RGRGSMGSE
SEQ ID NO:38      LASPKG-----QPPVAGGG-----ARQGLDEQVANK-----
SEQ ID NO:43      APSRPHYTNSYGGAGPGGDVYSLQSSKGVTPTRSNFEDEVMTAKKAGRGRGSMGSE
SEQ ID NO:44      ---GGRNSNF-----GPGEAVFG---SKGTPRPSNYEEDGGPA--KPTAAGTAGAG
360

244

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FIGURE 1 CONTINUED

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* * * * *
SEQ ID NO:14 -----EKGACGGGGGGHSPQQA-----VAVPAKRKDLHM
SEQ ID NO:30 -FHYHA-----AGTGHYPAPNPGMFSPNSKSVAAANAKRPNQOALPEQGNRLHM
SEQ ID NO:34 LFN-----GGLVSSNYPPNP-MFSGSTSAAGPKKKDSSGG-----GAVAPNKLHM
SEQ ID NO:38 -FK-----GGEAAAPYAPNP-GMM-----MPAPRKELGGSNS-----DKELHM
SEQ ID NO:43 LYN-----NNSVPS-YPPNP-MFTGSTSGAGSVKKKESGGGGGGVGVGQNKEMNM
SEQ ID NO:44 RFHYQSGGGGGGAHYAPAPNPGMSPNTGGGGTAAGNAPVVGK--RQDGNRDLHM
361 420

***** * *
SEQ ID NO:14 LVMSSASPVSE-----RAAVHVFAGGA-----DHADVLAQAQAYDEY---GRDDY
SEQ ID NO:30 FVWSSASPVSDV-----FGA-----HEYGGG--HDOKEVLNVSPGKVEN
SEQ ID NO:34 FVWSSASPVSEGNLRHAVNRAASTDFTGVPDSKAVPHETVASKAYHELITENNSPGRRS
SEQ ID NO:38 FVWSSASPVSEANLRNAVNHAASTDFAAAPPAATPRDGTGRGVSGSVTPVWKDASS
SEQ ID NO:43 FVWSSASPVSEANAKNAMTRGSDTVDTPKYSIPPHONLATKAMQNLITENNSPGRKH
SEQ ID NO:44 FVWSSASPVSDV-----FGGGGNNHADYSTATNDHQDKVKSIVPQGSND
481 480

*** *****
SEQ ID NO:14 SSKTKNGSGG-ADKGGPTLS-KLGSNSTAQLYPKD-----DGEGRAAAVAMPASPASVMTRLI
SEQ ID NO:30 NHRDT--QEDYLEKDEFFSGNR---EMDREMNOLEGEKVGDGK---PKTMPPASPASVMTRLI
SEQ ID NO:34 GEREPMDG-----AKIPASGSPYTCOKYDMEDGNAN-KNQOMPASPASVMTRLI
SEQ ID NO:38 GAVEVEIDGMMKSPATGLGAKFPVSGSPYVAPRKKGA DVPGLEEAHPMPASPASVMTRLI
SEQ ID NO:43 VEMDQDNG-----GK-----SPYMGKKGSDVEDGGPGRKQMPASPASVMTRLI
SEQ ID NO:44 NQ-----YVEREEFFSGNK---DDDSKVLATDGGNNISNKTQAKVMPPTSVMTRLI
481 540

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FIGURE 1 CONTINUED

SEQ ID NO:14
 SEQ ID NO:30
 SEQ ID NO:34
 SEQ ID NO:38
 SEQ ID NO:43
 SEQ ID NO:44

 LIMVWRKLI RNPNTYSS LIGVWMSLVSRWGIEMPAIIARSISILSDAGLGMAMFSLGLF
 LIMVWRKLI RNPNTYSS LIGITWLSVSKWNVEMPAIIAKSISILSDAGLGMAMFSLGLF
 LIMVWRKLI RNPNTYSS LLLGLTWLSIFRWHIEMPTIVKGSISILSDAGLGMAMFSLGLF
 LIMVWRKLI RNPNTYSS LIGLWMSLVSRWNIQWPTTIKGSISILSDAGLGMAMFSLGLF
 LIMVWRKLI RNPNTYSS LIFGLWMSLVSRWNIQWPTIIMSGSISILSDAGLGMAMFSLGLF
 LIMVWRKLI RNPNTYSS LFGITWLSIFRWHIEMPAIIAKSISILSDAGLGMAMFSLGLF

541

600

SEQ ID NO:14
 SEQ ID NO:30
 SEQ ID NO:34
 SEQ ID NO:38
 SEQ ID NO:43
 SEQ ID NO:44

 MALQPRIIACGNKLAATAMGVRFVAGPAMVMAAASIAVGLRGVLLHHTAIVOAALPQGI VPF
 MALQPRIIACGNSTAFAFAMAVRELTGPAMVMAAASIAVGLRGVLLHHTAIVOAALPQGI VPF
 MALQPRIIACGKSVAAFSMAVRELTGPVIAAATSIGIGLRGVLLHHTAIVOAALPQGI VPF
 MALQPRIIACGKSVATFAMAVRELTGPVIAAATSIGIGLRGVLLHHTAIVOAALPQGI VPF
 MALQPRIIACGKSVAGFAMAVRELTGPVIAAATSIGIGLRGVLLHHTAIVOAALPQGI VPF
 MALQPRIIACGNRRRAAFAMRFFVGPVAMVMAAASIAVGLRGVLLHHTAIVOAALPQGI VPF

601

660

SEQ ID NO:14
 SEQ ID NO:30
 SEQ ID NO:34
 SEQ ID NO:38
 SEQ ID NO:43
 SEQ ID NO:44

 VFAKEYGVHPDILSTA--YG-----PITSHGFITCS
 VFAKEYNVHPDILSTAVIFGMLIALPITLVIYLLGL
 VFAKEYNLHADILSTAVIFGMLIALPITLVIYLLGV
 VFAKEYNCHPOILSTAVIFGMLVALPITLVIYLLGI
 VFAKEYNVHPDILSTAVIFGMLVALPITLVIYLLGL
 VFAKEYNVHPDILSTAVIFGMLIALPITLVIYLLGL

661

697